

<110> Connaught Laboratories Limited

<120> Chlamydia antigens and corresponding DNA fragments and uses thereof

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<151> December 23, 1998

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<151> December 28, 1998

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<170> PatentIn Ver. 2.0

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 Gly Thr Ile Leu Phe Ser Gly Glu Lys Ser Leu Ala Asn Asp Pro Arg
 410 415 420

gat ttt aaa tct aca atc cct cag aac gtc aac ctg tct gca gga tac 1411
 Asp Phe Lys Ser Thr Ile Pro Gln Asn Val Asn Leu Ser Ala Gly Tyr
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tta gtt att aaa gag ggg gcc gaa gtc aca gtt tca aaa ttc acg cag 1459
 Leu Val Ile Lys Glu Gly Ala Glu Val Thr Val Ser Lys Phe Thr Gln
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 Ser Pro Gly Ser His Leu Val Leu Asp Leu Gly Thr Lys Leu Ile Ala
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tta agc tca tcc tca aca gca gct gtt att aaa gca aac acc gca aat 1603
 Leu Ser Ser Ser Ser Thr Ala Ala Val Ile Lys Ala Asn Thr Ala Asn
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aaa cag ata tcc gtg acg gac tct ata gaa ctt atc tcg cct act ggc 1651
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gat ttc cta ccg gta agt ccc cat tat ggt ttt caa ggc aat tgg aaa 1795
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Leu Ala Trp Thr Gly Thr Gly Asn Lys Val Gly Glu Phe Phe Trp Asp	
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aaa ata aat tat aag cct aga cct gaa aaa gaa gga aat tta gtt cct	1891
Lys Ile Asn Tyr Lys Pro Arg Pro Glu Lys Glu Gly Asn Leu Val Pro	
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Asn Ile Leu Trp Gly Asn Ala Val Asp Val Arg Ser Leu Met Gln Val	
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Gln Glu Thr His Ala Ser Ser Leu Gln Thr Asp Arg Gly Leu Trp Ile	
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Ile Thr Pro Lys His Tyr Thr Ser Met Ala Phe Ser Gln Leu Phe Ser	
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Tyr Ala Ser Arg Asn Pro Asn Val Asn Val Gly Ile Leu Ser Arg Arg	
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His Ala Thr Asn Asp Met Lys Thr Asp Tyr Ala Asn Phe Pro Met Val	
745 750 755	
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Lys Asn Ser Trp Arg Asn Asn Cys Trp Ala Ile Glu Cys Gly Gly Ser	
760 765 770	
atg cct cta ttg gta ttt gag aac gga aga ctt ttc caa ggt gcc atc	2467
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 890 895 900

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 Met Pro Ser Ser Trp
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aaa agg tta tta cag gtt ctg tct cac aaa ata gca gct aca gaa agt 163
 Lys Arg Leu Leu Gln Val Leu Ser His Lys Ile Ala Ala Thr Glu Ser
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ggt ggg ggt atc tac gct aag gat att caa cta caa gct cta cct gga 211
 Gly Gly Gly Ile Tyr Ala Lys Asp Ile Gln Leu Gln Ala Leu Pro Gly
 25 30 35

agc ttc aca att acc gat aat aaa gtc gaa act agt ctt act act agc 259
 Ser Phe Thr Ile Thr Asp Asn Lys Val Glu Thr Ser Leu Thr Thr Ser
 40 45 50

act aat tta tat ggt ggg ggc atc tat tcc agt gga gct gtc acg cta 307
 Thr Asn Leu Tyr Gly Gly Gly Ile Tyr Ser Ser Gly Ala Val Thr Leu
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acc aat ata tct gga acc ttt ggc att aca gga aac tct gtt atc aat 355
 Thr Asn Ile Ser Gly Thr Phe Gly Ile Thr Gly Asn Ser Val Ile Asn
 70 75 80 85

aca gcg aca tcc cag gat gca gat ata caa ggt ggg ggc att tat gca 403
 Thr Ala Thr Ser Gln Asp Ala Asp Ile Gln Gly Gly Gly Ile Tyr Ala
 90 95 100

acc acg tct ctc tca ata aat caa tgt aat aca ccc att cta ttt agc 451
 Thr Thr Ser Leu Ser Ile Asn Gln Cys Asn Thr Pro Ile Leu Phe Ser
 105 110 115

aac aac tct gct gcc act aaa aaa aca tca aca aca aag caa att gct 499
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 120 125 130

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 135 140 145

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 Pro Ile Ile Phe Leu Asn Asn Ser Ala Lys Ser Glu Ala Thr Thr Ala
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gca act gca gga aat aaa gat agc tgt gga gga gcc att gca gct aac 643
 Ala Thr Ala Gly Asn Lys Asp Ser Cys Gly Gly Ala Ile Ala Ala Asn
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tct gtt act tta aca aat aac cct gaa ata acc ttt aaa gga aat tat 691
 Ser Val Thr Leu Thr Asn Asn Pro Glu Ile Thr Phe Lys Gly Asn Tyr
 185 190 195

gca gaa act gga gga gcg att ggc tgt att gat ctt act aat ggc tca 739
 Ala Glu Thr Gly Gly Ala Ile Gly Cys Ile Asp Leu Thr Asn Gly Ser
 200 205 210

cct ccc cgt aaa gtc tct att gca gac aac ggt tct gtc ctt ttt caa 787
 Pro Pro Arg Lys Val Ser Ile Ala Asp Asn Gly Ser Val Leu Phe Gln
 215 220 225

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 230 235 240 245

gat atc tcc agg aca ggt gcg act ttc atc ggt aac tct tca aaa cat 883
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 250 255 260

gat gga agt gca att tgc tgt tca aca gcc cta act ctt gcg cca aac 931
 Asp Gly Ser Ala Ile Cys Cys Ser Thr Ala Leu Thr Leu Ala Pro Asn
 265 270 275

tcc caa ctt atc ttt gaa aac aat aag gtt acg gaa acc aca gcc act 979
 Ser Gln Leu Ile Phe Glu Asn Asn Lys Val Thr Glu Thr Thr Ala Thr
 280 285 290

aca aaa gct tcc ata aat aat tta gga gct gca att tat gga aat aat 1027
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 295 300 305

gag act agt gac gtc act atc tct tta tca gct gag aat gga agt att 1075
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 310 315 320 325

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 330 335 340

gct gga aac gta aaa ttt aca gca ata gaa gct tca gca ggg aaa gct 1171
 Ala Gly Asn Val Lys Phe Thr Ala Ile Glu Ala Ser Ala Gly Lys Ala
 345 350 355

ata tct ttc tat gat gca gtt aac gtt cca cca aag aaa caa ttg ctc 1219
 Ile Ser Phe Tyr Asp Ala Val Asn Val Pro Pro Lys Lys Gln Leu Leu
 360 365 370

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 Lys Ser
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cct Pro	tg Trp	cta Leu	ctt Leu	acc Thr 10	tct Ser	tcg Ser	gct Ala	tta Leu	gtt Val 15	ttc Phe	tcc Ser	cta Leu	cat His	cca Pro 20	cta Leu	163
atg Met	gct Ala	gct Ala	aac Asn 25	acg Thr	gat Asp	ctc Leu	tca Ser	tca Ser 30	tcc Ser	gat Asp	aac Asn	tat Tyr	gaa Glu 35	aat Asn	gg Gly	211
agt Ser	agt Ser	gg Gly 40	agc Ser	gca Ala	gca Ala	ttc Phe	act Thr 45	gcc Ala	aag Lys	gaa Glu	act Thr 50	tcg Ser	gat Asp	gct Ala	tca Ser	259
gga Gly	act Thr 55	acc Thr	tac Tyr	act Thr	ctc Leu	act Thr 60	agc Ser	gat Asp	gtt Val	tct Ser	att Ile 65	acg Thr	aat Asn	gta Val	tct Ser	307
gca Ala 70	att Ile	act Thr	cct Pro	gca Ala	gat Asp 75	aaa Lys	agc Ser	tgt Cys	ttt Phe	aca Thr 80	aac Asn	aca Thr	gga Gly	gga Gly	gca Ala 85	355
ttg Leu	agt Ser	ttt Phe	gtt Val 90	gga Gly	gct Ala	gat Asp	cac His	tca Ser	ttg Leu 95	gtt Val	ctg Leu	caa Gln	acc Thr	ata Ile 100	gcg Ala	403
ctt Leu	acg Thr	cat His	gat Asp 105	gg Gly	gct Ala	gca Ala	att Ile	aac Asn 110	aat Asn	acc Thr	aac Asn	aca Thr 115	gct Ala	ctt Leu	tct Ser	451
ttc Phe	tca Ser	gga Gly 120	ttc Phe	tcg Ser	tca Ser	ctc Leu	tta Leu 125	atc Ile	gac Asp	tca Ser	gct Ala 130	cca Pro	gca Ala	aca Thr	gga Gly	499
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act Thr 150	gcg Ala	act Thr	ttt Phe	act Thr	gac Asp 155	aat Asn	gcc Ala	agt Ser	gtc Val	acc Thr 160	ctc Leu	caa Gln	aaa Lys	aat Asn	act Thr 165	595
tca Ser	gaa Glu	aaa Lys	gat Asp	gga Gly 170	gct Ala	gca Ala	gtt Val	tct Ser	gcc Ala 175	tac Tyr	agc Ser	atc Ile	gat Asp	ctt Leu 180	gct Ala	643
aag Lys	act Thr	acg Thr	aca Thr 185	gca Ala	gct Ala	ctc Leu	tta Leu 190	gat Asp	caa Gln	aat Asn	act Thr 195	agc Ser	aca Thr	aaa Lys	aat Asn	691
ggc Gly	ggg Gly	gcc Ala 200	ctc Leu	tgt Cys	agt Ser	aca Thr	gca Ala 205	aac Asn	act Thr	aca Thr 210	gtc Val	caa Gln 210	gga Gly	aac Asn	tca Ser	739

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Gly Thr Val Thr Phe Ser Ser Asn Thr Ala Thr Asp Lys Gly Gly Gly	
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atc tac tca aaa gaa aag gat agc acg cta gat gcc aat aca gga gtc	835
Ile Tyr Ser Lys Glu Lys Asp Ser Thr Leu Asp Ala Asn Thr Gly Val	
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gtt acc ttc aaa tct aat act gca aag acg ggg ggt gct tgg agc tct	883
Val Thr Phe Lys Ser Asn Thr Ala Lys Thr Gly Gly Ala Trp Ser Ser	
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Asp Asp Asn Leu Ala Leu Thr Gly Asn Thr Gln Val Leu Phe Gln Glu	
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Thr Lys Cys Ala Leu His Gly Asn Thr Thr Leu Thr Phe Asp Gly Asn	
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615 620 625	
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aag aca gca ggg gct cta cat act aaa gga aat act tcc ttt acc aaa	2083
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SUBSTITUTE SHEET (RULE 26)

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Ser Glu Asn Lys Gly Asn Leu Ser Phe Glu Arg Asn Ser Ser His Ser
120 125 130

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Ser	Gly	Gly	Ala	Leu	Tyr	Ser	Val	Arg	Glu	Cys	Trp	Ile	Ser	Lys	Asn	
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Thr Ser Gly Phe Gly Gly Ala Ile His Ala Leu Asp Ser Tyr Ile Thr	
170 175 180	
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Asn Asn Leu Gly Glu Gly Gln Phe Leu Asp Asn Val Ser Lys Asn Arg	
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Gly Pro Ile Val Ile Lys Lys Asn Gln Thr Leu Glu Asp Ser Ser Phe	
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Asn Ile Gln Ile Asn Asp Asn Ala Ser Gly Gln Gly Val Val Tyr Phe	
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Leu Pro Leu Gly Val Ile Ile Ser Ser Asn Lys Glu Ile Ile Glu Ile	
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Pro Gly Gly Gly Ile Met Cys Thr Ser Leu Ser His Glu Asn Asn	
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Pro Lys Gly Leu Ile Phe Asn Asn Lys Thr Ala Ala Leu Ser Gly Gly	
310 315 320 325	
gta tac aca cga gat ctt tca tct tcc aaa ata acg gtc cgc aca gca	1123
Val Tyr Thr Arg Asp Leu Ser Ser Ser Lys Ile Thr Val Arg Thr Ala	
330 335 340	
ttt att aat aac tct gcg act tca gga ggg gct ctc atc aat ctt tct	1171
Phe Ile Asn Asn Ser Ala Thr Ser Gly Gly Ala Leu Ile Asn Leu Ser	
345 350 355	
ggt ata gga agt act cct caa aat ttc ttc ctc tct gca gac tac ggc	1219
Gly Ile Gly Ser Thr Pro Gln Asn Phe Phe Leu Ser Ala Asp Tyr Gly	
360 365 370	

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gat att cta ttt aac aat aat aca atc aca tct tct tct cct caa ccc	1267
Asp Ile Leu Phe Asn Asn Asn Thr Ile Thr Ser Ser Ser Pro Gln Pro	
375 380 385	
gga tat aga aat gca ctc tat gct gct ccg ggg att aac tta aaa cta	1315
Gly Tyr Arg Asn Ala Leu Tyr Ala Ala Pro Gly Ile Asn Leu Lys Leu	
390 395 400 405	
gga gca aga cag ggt tat aaa att ctc ttt tat gat cct ata gat cac	1363
Gly Ala Arg Gln Gly Tyr Lys Ile Leu Phe Tyr Asp Pro Ile Asp His	
410 415 420	
gat cag acg aca aca gat cct ata gta ttt aat tat gaa ccc cat cac	1411
Asp Gln Thr Thr Thr Asp Pro Ile Val Phe Asn Tyr Glu Pro His His	
425 430 435	
ctt ggc acc gtg ttg ttt tcc gga atc aat gta gat tct aac gca aca	1459
Leu Gly Thr Val Leu Phe Ser Gly Ile Asn Val Asp Ser Asn Ala Thr	
440 445 450	
aat cca ttg aac ttc cta tca aaa ttt tct aac tct tca cga ctt gaa	1507
Asn Pro Leu Asn Phe Leu Ser Lys Phe Ser Asn Ser Ser Arg Leu Glu	
455 460 465	
agg ggt gtg ctc gct att gaa gat cgg gct gct att tct tgc aaa acc	1555
Arg Gly Val Leu Ala Ile Glu Asp Arg Ala Ala Ile Ser Cys Lys Thr	
470 475 480 485	
cta tcg caa act ggg ggc att cta cgt tta gga aac gca gca tta atc	1603
Leu Ser Gln Thr Gly Gly Ile Leu Arg Leu Gly Asn Ala Ala Leu Ile	
490 495 500	
agg acg aaa ggc ccg gga agc tcc ata aat ttt aat gca atc gcg atc	1651
Arg Thr Lys Gly Pro Gly Ser Ser Ile Asn Phe Asn Ala Ile Ala Ile	
505 510 515	
aat ctt cct tct att tta caa tca gaa gcc tca gct cca aag ttc tgg	1699
Asn Leu Pro Ser Ile Leu Gln Ser Glu Ala Ser Ala Pro Lys Phe Trp	
520 525 530	
att tat cct aca tta aca gga tcc acc tat tct gaa gac act tct tct	1747
Ile Tyr Pro Thr Leu Thr Gly Ser Thr Tyr Ser Glu Asp Thr Ser Ser	
535 540 545	
act atc act ctc tca gga ccc ttg act ttt cta aac gat gaa aat gaa	1795
Thr Ile Thr Leu Ser Gly Pro Leu Thr Phe Leu Asn Asp Glu Asn Glu	
550 555 560 565	
aac ccc tat gat agc tta gat ctc tct gaa cct cga aag gat atc ccc	1843
Asn Pro Tyr Asp Ser Leu Asp Leu Ser Glu Pro Arg Lys Asp Ile Pro	
570 575 580	
cct cct cta cct cct cga tgt gac tgc aaa aaa atc gat act tcg aat	1891
Pro Pro Leu Pro Pro Arg Cys Asp Cys Lys Lys Ile Asp Thr Ser Asn	
585 590 595	

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ctc att gta gaa gcc atg aac tta gat gag cac tat gga tat cag gga 1939
 Leu Ile Val Glu Ala Met Asn Leu Asp Glu His Tyr Gly Tyr Gln Gly
 600 605 610

atc tgg tct ccc tat tgg atg gaa act acg act aca aca agc tct aca 1987
 Ile Trp Ser Pro Tyr Trp Met Glu Thr Thr Thr Thr Thr Ser Ser Thr
 615 620 625

gta ccg gaa cag acc aat aca aac cac agg cag ctc tac gta gac tgg 2035
 Val Pro Glu Gln Thr Asn Thr Asn His Arg Gln Leu Tyr Val Asp Trp
 630 635 640 645

act cct gta gga tac cgc cct aac ccg gaa cgt cac gga gaa ttt att 2083
 Thr Pro Val Gly Tyr Arg Pro Asn Pro Glu Arg His Gly Glu Phe Ile
 650 655 660

gct aat acc tta tgg cag tct gcc tat aac gct ctg tta gga atc cgc 2131
 Ala Asn Thr Leu Trp Gln Ser Ala Tyr Asn Ala Leu Leu Gly Ile Arg
 665 670 675

atc tta cct cca caa aac ctc aaa gag cat gac ctt gaa gcc tct ctg 2179
 Ile Leu Pro Pro Gln Asn Leu Lys Glu His Asp Leu Glu Ala Ser Leu
 680 685 690

caa gga ctc ggg ctt cta att aac caa cat aat cgc gag gga cgc aaa 2227
 Gln Gly Leu Gly Leu Leu Ile Asn Gln His Asn Arg Glu Gly Arg Lys
 695 700 705

ggc ttc cga aac cat act acg ggc tat gca gca aca acc tca gca aaa 2275
 Gly Phe Arg Asn His Thr Thr Gly Tyr Ala Ala Thr Thr Ser Ala Lys
 710 715 720 725

act gca gca cga cat agt ttc tct tta gga ttc gca caa atg ttc tcc 2323
 Thr Ala Ala Arg His Ser Phe Ser Leu Gly Phe Ala Gln Met Phe Ser
 730 735 740

aaa act aga gaa cgt caa tct cca agt acg act tcc tcc cac aac tac 2371
 Lys Thr Arg Glu Arg Gln Ser Pro Ser Thr Thr Ser Ser His Asn Tyr
 745 750 755

ttt gca gga ctc cgc ttc gac agt ctc ctc ttc agg gac ttc atc tct 2419
 Phe Ala Gly Leu Arg Phe Asp Ser Leu Leu Phe Arg Asp Phe Ile Ser
 760 765 770

aca ggg cta tcc cta ggt tat agc tac gga gat cac cat atg ctt tgc 2467
 Thr Gly Leu Ser Leu Gly Tyr Ser Tyr Gly Asp His His Met Leu Cys
 775 780 785

cac tat aca gaa atc tta aaa ggg tcg tcc aaa gcc ttc ttt aat aac 2515
 His Tyr Thr Glu Ile Leu Lys Gly Ser Ser Lys Ala Phe Phe Asn Asn
 790 795 800 805

cac act ttg gta gcc tct cta gac tgc aca ttc tta cca gct aga atc 2563
 His Thr Leu Val Ala Ser Leu Asp Cys Thr Phe Leu Pro Ala Arg Ile
 810 815 820

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acc cgc act ctc gaa ctc cag ccc ttt atc agt gcc att gct ctg cgc 2611
 Thr Arg Thr Leu Glu Leu Gln Pro Phe Ile Ser Ala Ile Ala Leu Arg
 825 830 835

tgt tcc cag gcc tcg ttc caa gaa act gga gac cat ata aga aaa ttc 2659
 Cys Ser Gln Ala Ser Phe Gln Glu Thr Gly Asp His Ile Arg Lys Phe
 840 845 850

cat cca aaa cat ccc ctt aca gat ctt tcc tct ccc ata ggc ttc cgt 2707
 His Pro Lys His Pro Leu Thr Asp Leu Ser Ser Pro Ile Gly Phe Arg
 855 860 865

tct gaa tgg aaa act tca cat cat atc ccc atg cta tgg act acg gaa 2755
 Ser Glu Trp Lys Thr Ser His His Ile Pro Met Leu Trp Thr Thr Glu
 870 875 880 885

ata tcc tac gta cct acc cta tac aga aaa aat cca gaa atg ttc acg 2803
 Ile Ser Tyr Val Pro Thr Leu Tyr Arg Lys Asn Pro Glu Met Phe Thr
 890 895 900

aca cta ctc atc agc aat gga aca tgg aca aca caa gca act ccc gtc 2851
 Thr Leu Leu Ile Ser Asn Gly Thr Trp Thr Thr Gln Ala Thr Pro Val
 905 910 915

tcc tat aat tcc gta gct gca aaa ata aaa aat act tcc caa ctt ttc 2899
 Ser Tyr Asn Ser Val Ala Ala Lys Ile Lys Asn Thr Ser Gln Leu Phe
 920 925 930

tca aga gta acc tta tcc tta gat tat tca gct caa gtc tcc tcg tca 2947
 Ser Arg Val Thr Leu Ser Leu Asp Tyr Ser Ala Gln Val Ser Ser Ser
 935 940 945

act gta ggt caa tac ctt aaa gct gag agt cat tgc aca ttt 2989
 Thr Val Gly Gln Tyr Leu Lys Ala Glu Ser His Cys Thr Phe
 950 955 960

taaccacaaa gaaaacatca aggaataaac agtgcaaaat aacagatccc ttagtaaate 3049

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 <211> 1745
 <212> DNA
 <213> Chlamydia pneumoniae

<220>
 <221> CDS
 <222> (101)..(1642)

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 attaaagttg cttcaacctt attgatttaa cgaggaaacc atg acc ata ctt cga 115

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	Met	Thr	Ile	Leu	Arg	
	1				5	
aat ttt ctt acc tgc tcg gct tta ttc ctc gct ctc cct gca gca gca						163
Asn Phe Leu Thr Cys Ser Ala Leu Phe Leu Ala Leu Pro Ala Ala Ala						
	10			15	20	
caa gtt gta tat ctt cat gaa agt gat ggt tat aac ggt gct atc aat						211
Gln Val Val Tyr Leu His Glu Ser Asp Gly Tyr Asn Gly Ala Ile Asn						
	25			30	35	
aat aaa agc tta gaa cct aaa att acc tgt tat cca gaa gga act tct						259
Asn Lys Ser Leu Glu Pro Lys Ile Thr Cys Tyr Pro Glu Gly Thr Ser						
	40			45	50	
tac atc ttt cta gat gac gtg agg att tcc aac gtt aag cat gat caa						307
Tyr Ile Phe Leu Asp Asp Val Arg Ile Ser Asn Val Lys His Asp Gln						
	55			60	65	
gaa gat gct ggg gtt ttt ata aat cga tct ggg aat ctt ttt ttc atg						355
Glu Asp Ala Gly Val Phe Ile Asn Arg Ser Gly Asn Leu Phe Phe Met						
	70			75	80	85
ggc aac cgt tgc aac ttc act ttt cac aac ctt atg acc gag ggt ttt						403
Gly Asn Arg Cys Asn Phe Thr Phe His Asn Leu Met Thr Glu Gly Phe						
	90			95	100	
ggc gct gcc att tcg aac cgc gtt gga gac acc act ctc act ctc tct						451
Gly Ala Ala Ile Ser Asn Arg Val Gly Asp Thr Thr Leu Thr Leu Ser						
	105			110	115	
aat ttt tct tac tta gcg ttc acc tca gca cct cta cta cct caa gga						499
Asn Phe Ser Tyr Leu Ala Phe Thr Ser Ala Pro Leu Leu Pro Gln Gly						
	120			125	130	
caa gga gcg att tat agt ctt ggt tcc gtg atg atc gaa aat agt gag						547
Gln Gly Ala Ile Tyr Ser Leu Gly Ser Val Met Ile Glu Asn Ser Glu						
	135			140	145	
gaa gtg act ttc tgt ggg aac tac tct tcg tgg agt gga gct gcg att						595
Glu Val Thr Phe Cys Gly Asn Tyr Ser Ser Trp Ser Gly Ala Ala Ile						
	150			155	160	165
tat act ccc tac ctt tta ggt tct aag gcg agt cgt cct tca gta aat						643
Tyr Thr Pro Tyr Leu Leu Gly Ser Lys Ala Ser Arg Pro Ser Val Asn						
	170			175	180	
ctc agc ggg aac cgc tac ctg gtg ttt aga gac aat gtg agc caa gtt						691
Leu Ser Gly Asn Arg Tyr Leu Val Phe Arg Asp Asn Val Ser Gln Val						
	185			190	195	
tat ggc ggc gcc ata tct acc cac aat ctc aca ctc acg act cga gga						739
Tyr Gly Gly Ala Ile Ser Thr His Asn Leu Thr Leu Thr Arg Gly						
	200			205	210	

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cct tcg tgt ttt gaa aat aat cat gct tat cat gac gtg aat agt aat	787
Pro Ser Cys Phe Glu Asn Asn His Ala Tyr His Asp Val Asn Ser Asn	
215 220 225	
gga gga gcc att gcc att gct cct gga gga tcg atc tct ata tcc gtg	835
Gly Gly Ala Ile Ala Ile Ala Pro Gly Gly Ser Ile Ser Ile Ser Val	
230 235 240 245	
aaa agc gga gat ctc atc ttc aaa gga aat aca gca tca caa gac gga	883
Lys Ser Gly Asp Leu Ile Phe Lys Gly Asn Thr Ala Ser Gln Asp Gly	
250 255 260	
aat aca ata cac aac tcc atc cat ctg caa tct gga gca cag ttt aag	931
Asn Thr Ile His Asn Ser Ile His Leu Gln Ser Gly Ala Gln Phe Lys	
265 270 275	
aac cta cgt gct gtt tca gaa tcc gga gtt tat ttc tat gat cct ata	979
Asn Leu Arg Ala Val Ser Glu Ser Gly Val Tyr Phe Tyr Asp Pro Ile	
280 285 290	
agc cat agc gag tcg cat aaa att aca gat ctt gta atc aat gct cct	1027
Ser His Ser Glu Ser His Lys Ile Thr Asp Leu Val Ile Asn Ala Pro	
295 300 305	
gaa gga aag gaa act tat gaa gga aca att agc ttc tca gga cta tgc	1075
Glu Gly Lys Glu Thr Tyr Glu Gly Thr Ile Ser Phe Ser Gly Leu Cys	
310 315 320 325	
ctg gat gat cat gaa gtt tgt gcg gaa aat ctt act tcc aca atc cta	1123
Leu Asp Asp His Glu Val Cys Ala Glu Asn Leu Thr Ser Thr Ile Leu	
330 335 340	
caa gat gtc aca tta gca gga gga act ctc tct cta tcg gat ggg gtt	1171
Gln Asp Val Thr Leu Ala Gly Gly Thr Leu Ser Leu Ser Asp Gly Val	
345 350 355	
acc ttg caa ctg cat tct ttt aag cag gaa gca agc tct acg ctt act	1219
Thr Leu Gln Leu His Ser Phe Lys Gln Glu Ala Ser Ser Thr Leu Thr	
360 365 370	
atg tct cca gga acc act ctg ctc tgc tca gga gat gct cgg gtt cag	1267
Met Ser Pro Gly Thr Thr Leu Leu Cys Ser Gly Asp Ala Arg Val Gln	
375 380 385	
aat ctg cac atc ctg att gaa gat acc gac aac ttt gtt cct gta agg	1315
Asn Leu His Ile Leu Ile Glu Asp Thr Asp Asn Phe Val Pro Val Arg	
390 395 400 405	
att cgc gcc gag gac aag gat gct ctt gtc tca tta gaa aaa ctt aaa	1363
Ile Arg Ala Glu Asp Lys Asp Ala Leu Val Ser Leu Glu Lys Leu Lys	
410 415 420	
gtt gcc ttt gag gct tat tgg tcc gtc tat gac ttt cct caa ttt aag	1411
Val Ala Phe Glu Ala Tyr Trp Ser Val Tyr Asp Phe Pro Gln Phe Lys	
425 430 435	

gaa gcc ttt acg att cct ctt gaa ctt cta ggg cct tct ttt gac	1459
Glu Ala Phe Thr Ile Pro Leu Leu Glu Leu Leu Gly Pro Ser Phe Asp	
440 445 450	
agt ctt ctc cta ggg gag acc act ttg gag aga acc caa gtc aca aca	1507
Ser Leu Leu Leu Gly Glu Thr Thr Leu Glu Arg Thr Gln Val Thr Thr	
455 460 465	
gag aat gac gcc gtt cga ggt ttc tgg tcc cta agc tgg gaa gag tac	1555
Glu Asn Asp Ala Val Arg Gly Phe Trp Ser Leu Ser Trp Glu Glu Tyr	
470 475 480 485	
ccc cct tct ctg gat aaa gac aga agg atc aca cca act aag aaa act	1603
Pro Pro Ser Leu Asp Lys Asp Arg Arg Ile Thr Pro Thr Lys Lys Thr	
490 495 500	
gtt ttc ctc act tgg aat cct gag atc act tct acg cca taatctctaa	1652
Val Phe Leu Thr Trp Asn Pro Glu Ile Thr Ser Thr Pro	
505 510	
gtctacacta taattaaggg aatcccccttt aagaagattt tgggacctat ctgtattcag	1712
agataggtcc ctctatgcac acatgttcac gag	1745
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<211> 1100	
<212> DNA	
<213> Chlamydia pneumoniae	
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<221> CDS	
<222> (101)..(967)	
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cagattttcc aaaacttcta taaatggaaa taaagagctt atg gga atc tct cta	115
Met Gly Ile Ser Leu	
1 5	
cca gag ctt ttt tcc aac cta ggt tct gct tac tta gat tat atc ttt	163
Pro Glu Leu Phe Ser Asn Leu Gly Ser Ala Tyr Leu Asp Tyr Ile Phe	
10 15 20	
caa cat cct ccg gcc tat gtt tgg tca gtt ttt ctt ctt tta tta gcc	211
Gln His Pro Pro Ala Tyr Val Trp Ser Val Phe Leu Leu Leu Leu Ala	
25 30 35	
cgt ctg ctt cct att ttt gct gta gct ccc ttc tta gga gca aag ctc	259
Arg Leu Leu Pro Ile Phe Ala Val Ala Pro Phe Leu Gly Ala Lys Leu	
40 45 50	
ttt ccc tcc cct att aaa atc ggg att agt ctc tct tgg ctt gca atc	307
Phe Pro Ser Pro Ile Lys Ile Gly Ile Ser Leu Ser Trp Leu Ala Ile	
55 60 65	

30/55

atc ttt cca aaa gtc ttg gcg gat acg cag atc aca aat tac atg gat 355
 Ile Phe Pro Lys Val Leu Ala Asp Thr Gln Ile Thr Asn Tyr Met Asp
 70 75 80 85

aac aat ctc ttt tat gtt tta ctt gtg aag gag atg atc ata ggc att 403
 Asn Asn Leu Phe Tyr Val Leu Leu Val Lys Glu Met Ile Ile Gly Ile
 90 95 100

gtg ata ggc ttt gtt tta gca ttt ccc ttt tat gct gca caa tgc gca 451
 Val Ile Gly Phe Val Leu Ala Phe Pro Phe Tyr Ala Ala Gln Ser Ala
 105 110 115

gga tct ttc atc act aac caa caa ggg att cag ggt tta gag ggc gcg 499
 Gly Ser Phe Ile Thr Asn Gln Gln Gly Ile Gln Gly Leu Glu Gly Ala
 120 125 130

aca tcc ctg att tcc att gag cag acc tct ccg cat ggc att tta tac 547
 Thr Ser Leu Ile Ser Ile Glu Gln Thr Ser Pro His Gly Ile Leu Tyr
 135 140 145

cat tac ttc gtg act att att ttt tgg tta gtg ggt ggt cac cgt att 595
 His Tyr Phe Val Thr Ile Ile Phe Trp Leu Val Gly Gly His Arg Ile
 150 155 160 165

gta atc tct ttg tta ttg caa act ctt gaa gtc att ccg atc cat agt 643
 Val Ile Ser Leu Leu Leu Gln Thr Leu Glu Val Ile Pro Ile His Ser
 170 175 180

ttc ttt cct gcc gag atg atg agc tta agt gcc ccg att tgg att act 691
 Phe Phe Pro Ala Glu Met Met Ser Leu Ser Ala Pro Ile Trp Ile Thr
 185 190 195

atg atc aag atg tgc cag ctc tgt ctc gtg atg acc ata cag ctg agt 739
 Met Ile Lys Met Cys Gln Leu Cys Leu Val Met Thr Ile Gln Leu Ser
 200 205 210

gct cct gca gct ttg gcg atg tta atg tcc gac cta ttc tta ggg att 787
 Ala Pro Ala Ala Leu Ala Met Leu Met Ser Asp Leu Phe Leu Gly Ile
 215 220 225

att aac cgt atg gca cct caa gtt cag gtc atc tac ctc ctc tct gcc 835
 Ile Asn Arg Met Ala Pro Gln Val Gln Val Ile Tyr Leu Leu Ser Ala
 230 235 240 245

ctt aag gct ttc atg ggt ctt ctc ttt ctc acc ctg gcg tgg tgg ttc 883
 Leu Lys Ala Phe Met Gly Leu Leu Phe Leu Thr Leu Ala Trp Trp Phe
 250 255 260

ata att aag cag ata gat tat ttc act ctt gct tgg ttc aaa gaa gtc 931
 Ile Ile Lys Gln Ile Asp Tyr Phe Thr Leu Ala Trp Phe Lys Glu Val
 265 270 275

ccc att atg ctc cta ggt tcc aac cct caa gta ctc taatcccccta 977
 Pro Ile Met Leu Leu Gly Ser Asn Pro Gln Val Leu
 280 285

31/55

ggctcttatac gtgactctta tctggagatg cgctcactta cgaatcttag cgcactgttt 1037
 atggattatac ttagggaatc tctcgcatat tcttttgtaa tctaagaatc tataaattca 1097
 aga 1100

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 <213> Chlamydia pneumoniae

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cttagtgact gccaacactt ttggaactct agacatcttg atg aag cac tcc aag 115
 Met Lys His Ser Lys
 1 5

gaa gat gac ctc tcc agg ttt ctt cct aaa aat ctt ctt gtt gaa tct 163
 Glu Asp Asp Leu Ser Arg Phe Leu Pro Lys Asn Leu Leu Val Glu Ser
 10 15 20

cct cat ccc gaa gaa atc cct tta aaa tct tta tct ttt acg atg agt 211
 Pro His Pro Glu Glu Ile Pro Leu Lys Ser Leu Ser Phe Thr Met Ser
 25 30 35

tgg cta cct aca att cat cct tca tgg att acc att gcc atg aaa gag 259
 Trp Leu Pro Thr Ile His Pro Ser Trp Ile Thr Ile Ala Met Lys Glu
 40 45 50

ttc cct cct gaa atc caa ggt caa tta tta gcg tgg ttg cca gag cct 307
 Phe Pro Pro Glu Ile Gln Gly Gln Leu Leu Ala Trp Leu Pro Glu Pro
 55 60 65

tta gtt caa gaa att cta ccc tta ctg cct ggc atc tct ata gcc cca 355
 Leu Val Gln Glu Ile Leu Pro Leu Leu Pro Gly Ile Ser Ile Ala Pro
 70 75 80 85

cat cgc tgt gca cct ttc gga gcc ttc tat ctt cta gat atg cta agt 403
 His Arg Cys Ala Pro Phe Gly Ala Phe Tyr Leu Leu Asp Met Leu Ser
 90 95 100

aaa aag atc cgt cct tgt gga att aca gaa gaa atc ttt ctt cct gca 451
 Lys Lys Ile Arg Pro Cys Gly Ile Thr Glu Glu Ile Phe Leu Pro Ala
 105 110 115

tcc tca gca aat gct ata ctt tac tat aca ggt cct gta aag atc gct 499
 Ser Ser Ala Asn Ala Ile Leu Tyr Tyr Thr Gly Pro Val Lys Ile Ala
 120 125 130

32/55

tta atc aac tgc cta ggt ctt tat tct att gct aaa gag ttg aag cac 547
 Leu Ile Asn Cys Leu Gly Leu Tyr Ser Ile Ala Lys Glu Leu Lys His
 135 140 145

att ctg gat aag gtt gtg att gaa cga gtg aag aat gct .ctc tcc cct 595
 Ile Leu Asp Lys Val Val Ile Glu Arg Val Lys Asn Ala Leu Ser Pro
 150 155 160 165

aca gag aaa ctc ttt ctt acc tac tgc caa tct cat ccg atg aaa cat 643
 Thr Glu Lys Leu Phe Leu Thr Tyr Cys Gln Ser His Pro Met Lys His
 170 175 180

tta gaa act acg aat ttt ctt tct tct tgg act act gat gca gaa tta 691
 Leu Glu Thr Thr Asn Phe Leu Ser Ser Trp Thr Thr Asp Ala Glu Leu
 185 190 195

cga cag ttc gtt cat aag caa ggg tta gag ttt tta ggt aaa gca tta 739
 Arg Gln Phe Val His Lys Gln Gly Leu Glu Phe Leu Gly Lys Ala Leu
 200 205 210

aca aaa gaa aac gct tct ttt cta tgg tat ttt cta cgt agg tta gat 787
 Thr Lys Glu Asn Ala Ser Phe Leu Trp Tyr Phe Leu Arg Arg Leu Asp
 215 220 225

gtc ggt cga gca tat atc gtc gag cag act tta aaa aca tgg tat gac 835
 Val Gly Arg Ala Tyr Ile Val Glu Gln Thr Leu Lys Thr Trp Tyr Asp
 230 235 240 245

cat ccc tat gtg gat tat ttt aag tcc cgc cta gaa caa tgc atg aaa 883
 His Pro Tyr Val Asp Tyr Phe Lys Ser Arg Leu Glu Gln Cys Met Lys
 250 255 260

gtc tta gtg aaa taaaagcttt ataagtaaag atttagcttt atacaaagta 935
 Val Leu Val Lys
 265

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 <213> Chlamydia pneumoniae

<220>
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tccaagggct tatgatcagc tttaaataag gacacgtgcc atg tta gca ttt ttc 115
 Met Leu Ala Phe Phe
 1 5

33/55

gca act agt ttc aaa tct gtt ctt ttt gag tac tcc tac caa tca tta 163
Ala Thr Ser Phe Lys Ser Val Leu Phe Glu Tyr Ser Tyr Gln Ser Leu
10 15 20

tta ctt att ttg att gtt tcg gca cct ccc atc atc tta gct tcc ata 211
Leu Leu Ile Leu Ile Val Ser Ala Pro Pro Ile Ile Leu Ala Ser Ile
25 30 35

gtc ggg att atg gtt gcg atc ttc caa gcc gca aca caa atc caa gaa 259
Val Gly Ile Met Val Ala Ile Phe Gln Ala Ala Thr Gln Ile Gln Glu
40 45 50

cag acc ttc gct ttt gca gtc aaa cta gtc gtg att ttt gga acc tta 307
Gln Thr Phe Ala Phe Ala Val Lys Leu Val Val Ile Phe Gly Thr Leu
55 60 65

atg atc tct gga ggg tgg ctt agc aat atg att tta cgc ttt gca ggt 355
Met Ile Ser Gly Gly Trp Leu Ser Asn Met Ile Leu Arg Phe Ala Gly
70 75 80 85

cag att ttc caa aac ttc tat aaa tgg aaa taaagagctt atgggaatct 405
Gln Ile Phe Gln Asn Phe Tyr Lys Trp Lys
90 95

ctctaccaga gcttttttcc aacctagggtt ctgcttactt agattatatc tttcaacatc 465

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<210> 14

<211> 552

<212> PRT

<213> Chlamydia pneumoniae

<400> 14

Met Val Ser Ser Pro Ile Leu Asn Val Pro Leu Lys Asn His Ala Ser
1 5 10 15

Val Ser Gly Lys Phe Thr His Arg Glu Val Ser Lys Leu Ala Ser Asp
20 25 30

Leu Lys Ser Gly Ala Met Ser Phe Val Pro Glu Val Leu Ser Glu Glu
35 40 45

Thr Ile Ser Ser Asp Leu Gly Lys Lys Gln Cys Thr Gln Gly Ile Ile
50 55 60

Ser Ala Cys Cys Gly Leu Ala Met Leu Ile Val Leu Met Ser Val Tyr
65 70 75 80

Tyr Arg Phe Gly Gly Val Ile Ala Ser Gly Ala Val Leu Leu Asn Leu
85 90 95

Leu Leu Ile Trp Ala Ala Leu Gln Tyr Leu Asp Ala Pro Leu Thr Leu
100 105 110

34/55

Ser Gly Leu Ala Gly Ile Val Leu Ala Met Gly Met Ala Val Asp Ala
 115 120 125
 Asn Val Leu Val Phe Glu Arg Ile Arg Glu Glu Phe Leu Leu Ser Gln
 130 135 140
 Ser Leu Lys Lys Ser Val Glu Lys Gly Tyr Thr Lys Ala Phe Gly Ala
 145 150 155 160
 Ile Phe Asp Ser Asn Leu Thr Thr Val Leu Ala Ser Ala Leu Leu Phe
 165 170 175
 Phe Leu Asp Thr Gly Pro Ile Lys Gly Phe Ala Leu Thr Leu Ile Leu
 180 185 190
 Gly Ile Phe Ser Ser Met Phe Thr Ala Leu Phe Met Thr Lys Phe Phe
 195 200 205
 Phe Met Leu Trp Met Asn Lys Thr Gln His Thr Gln Leu His Met Met
 210 215 220
 Asn Lys Phe Val Gly Ile Lys His Asp Phe Leu Arg Gly Cys Lys Lys
 225 230 235 240
 Leu Trp Ala Val Ser Gly Ser Val Phe Leu Leu Gly Cys Val Ala Leu
 245 250 255
 Gly Phe Gly Ala Trp Asn Ser Val Leu Gly Met Asp Phe Lys Gly Gly
 260 265 270
 Tyr Ala Phe Thr Phe Asn Pro Lys Glu His Gly Ile Ser Asp Val Ala
 275 280 285
 Gln Met Arg Gly Lys Val Val His Lys Leu Gln Glu Ala Gly Leu Ser
 290 295 300
 Ser Arg Asp Phe Arg Ile Gln Thr Phe Gly Ser Ser Glu Lys Ile Lys
 305 310 315 320
 Ile Tyr Phe Ser Asp Lys Ala Leu Ser Tyr Thr Lys Gln Ile Arg Ala
 325 330 335
 Ser Leu Leu Lys Leu Thr Ile Met Ser Trp Arg Tyr Cys Gly Ile Val
 340 345 350
 Val Arg Asn Arg Pro Arg Phe Leu Tyr Gly Asn Ser Lys Arg Asn Ala
 355 360 365
 Lys Phe Trp Ser Lys Val Ser Ser Lys Leu Ser Lys Lys Met Arg Tyr
 370 375 380
 Gln Ala Thr Ile Gly Leu Leu Gly Ala Leu Ala Ile Ile Leu Leu Tyr
 385 390 395 400

35/55

Val Ser Leu Arg Phe Glu Trp Gln Tyr Ala Phe Ser Ala Val Cys Ala
 405 410 415
 Leu Ile His Asp Leu Leu Ala Thr Cys Ala Val Leu Phe Ile Ala His
 420 425 430
 Phe Phe Leu Lys Lys Ile Gln Ile Asp Leu Gln Ala Ile Gly Ala Leu
 435 440 445
 Met Thr Val Leu Gly Tyr Ser Leu Asn Asn Thr Leu Ile Ile Phe Asp
 450 455 460
 Arg Ile Arg Glu Asp Arg Gln Ala Asn Leu Phe Thr Pro Met His Val
 465 470 475 480
 Leu Val Asn Asp Ala Leu Gln Lys Thr Phe Ser Arg Thr Val Met Thr
 485 490 495
 Thr Ala Thr Thr Leu Ser Val Leu Leu Met Leu Leu Phe Ile Gly Gly
 500 505 510
 Ser Ser Val Phe Asn Phe Ala Phe Ile Met Thr Ile Gly Ile Leu Leu
 515 520 525
 Gly Thr Leu Ser Ser Leu Tyr Ile Ala Pro Pro Leu Leu Leu Phe Met
 530 535 540
 Val Arg Lys Glu Asn Arg Ser Lys
 545 550
 <210> 15
 <211> 196
 <212> PRT
 <213> Chlamydia pneumoniae
 <400> 15
 Met Ser Ser Asn Leu His Pro Val Gly Gly Thr Gly Thr Gly Ala Ala
 1 5 10 15
 Ala Pro Glu Ser Val Leu Asn Ile Val Glu Glu Ile Ala Ala Ser Gly
 20 25 30
 Ser Val Thr Ala Gly Leu Gln Ala Ile Thr Ser Ser Pro Gly Met Val
 35 40 45
 Asn Leu Leu Ile Gly Trp Ala Lys Thr Lys Phe Ile Gln Pro Ile Arg
 50 55 60
 Glu Ser Lys Leu Phe Gln Ser Arg Ala Cys Gln Ile Thr Leu Leu Val
 65 70 75 80
 Leu Gly Ile Leu Leu Val Val Ala Gly Leu Ala Cys Met Phe Ile Phe
 85 90 95

36/55

His Ser Gln Leu Gly Ala Asn Ala Phe Trp Leu Ile Ile Pro Ala Ala
 100 105 110
 Ile Gly Leu Ile Lys Leu Leu Val Thr Ser Leu Cys Phe Asp Glu Ala
 115 120 125
 Cys Thr Ser Glu Lys Leu Met Val Phe Gln Lys Trp Ala Gly Val Leu
 130 135 140
 Glu Asp Gln Leu Asp Asp Gly Ile Leu Asn Asn Ser Asn Lys Ile Phe
 145 150 155 160
 Gly His Val Lys Thr Glu Gly Asn Thr Ser Arg Ala Thr Thr Pro Val
 165 170 175
 Leu Asn Asp Gly Arg Gly Thr Pro Val Leu Ser Pro Leu Val Ser Lys
 180 185 190
 Ile Ala Arg Val
 195
 <210> 16
 <211> 245
 <212> PRT
 <213> Chlamydia pneumoniae
 <400> 16
 Met Thr Ile Arg Ile Leu Ala Glu Gly Leu Ala Phe Arg Tyr Gly Ser
 1 5 10 15
 Lys Gly Pro Asn Ile Ile His Asp Val Ser Phe Ser Val Tyr Asp Gly
 20 25 30
 Asp Phe Ile Gly Ile Ile Gly Pro Asn Gly Gly Gly Lys Ser Thr Leu
 35 40 45
 Thr Met Leu Ile Leu Gly Leu Leu Thr Pro Thr Phe Gly Ser Leu Lys
 50 55 60
 Thr Phe Pro Ser His Ser Ala Gly Lys Gln Thr His Ser Met Ile Gly
 65 70 75 80
 Trp Val Pro Gln His Phe Ser Tyr Asp Pro Cys Phe Pro Ile Ser Val
 85 90 95
 Lys Asp Val Val Leu Ser Gly Arg Leu Ser Gln Leu Ser Trp His Gly
 100 105 110
 Lys Tyr Lys Lys Lys Asp Phe Glu Ala Val Asp His Ala Leu Asp Leu
 115 120 125
 Val Gly Leu Ser Asp Thr Thr Thr Ala Phe Ala His Leu Ser Gly
 130 135 140
 Gly Gln Ile Gln Arg Val Leu Leu Ala Arg Ala Leu Ala Ser Tyr Pro
 145 150 155 160

37/55

Glu Ile Leu Ile Leu Asp Glu Pro Thr Thr Asn Ile Asp Pro Asp Asn
 165 170 175

Gln Gln Arg Ile Leu Ser Ile Leu Lys Lys Leu Asn Arg Thr Cys Thr
 180 185 190

Ile Leu Met Val Thr His Asp Leu His His Thr Thr Asn Tyr Phe Asn
 195 200 205

Lys Val Phe Tyr Met Asn Lys Thr Leu His Phe Ile Gly Arg His Phe
 210 215 220

Asp Leu Asn Arg Pro Ile Leu Leu Ser Ser Tyr Lys Asn Gln Glu Phe
 225 230 235 240

Ser Cys Ser Pro His
 245

<210> 17
 <211> 278
 <212> PRT
 <213> Chlamydia pneumoniae

<400> 17
 Met His Lys Val Ile Val Phe Ile Phe Leu Thr Leu Tyr Ser Leu Lys
 1 5 10 15

Ser Tyr Gly Asn Asp Val Ile Asp Lys Pro His Val Leu Val Ser Ile
 20 25 30

Ala Pro Tyr Lys Phe Leu Val Glu Gln Ile Ala Glu Glu Thr Cys Phe
 35 40 45

Val Tyr Ala Ile Val Thr Asn His Tyr Asp Pro His Thr Tyr Glu Leu
 50 55 60

Pro Pro Gln Gln Ile Lys Glu Leu Arg Gln Gly Asp Leu Trp Phe Arg
 65 70 75 80

Ile Gly Glu Ala Phe Gly Lys Asn Leu Leu Glu Lys Pro Tyr Met Gln
 85 90 95

Gln Val Asp Leu Ser Gln Asn Val Ser Leu Ile Gln Gly Lys Pro Cys
 100 105 110

Cys Asn Gln His Thr Thr Asn Tyr Asp Thr His Thr Trp Leu Ser Pro
 115 120 125

Lys Asn Leu Lys Val Gln Val Glu Thr Ile Val Thr Thr Leu Ser Lys
 130 135 140

38/55

Lys Tyr Pro Gln His Ala Thr Leu Tyr Gln Ser Asn Gly Glu Lys Leu
 145 150 155 160
 Leu Leu Ala Leu Asp Gln Leu Asn Glu Glu Ile Leu Thr Ile Thr Ser
 165 170 175
 Lys Ala Lys Gln Arg His Ile Leu Val Ser His Gly Ala Phe Gly Tyr
 180 185 190
 Phe Cys Arg Asp Tyr Asn Phe Ser Gln His Thr Ile Glu Lys Ser Ser
 195 200 205
 His Val Glu Pro Ser Pro Lys Asp Val Ala Arg Val Phe Arg Asp Ile
 210 215 220
 Glu Gln Tyr Lys Ile Ser Ser Val Ile Leu Leu Glu Tyr Ser Gly Arg
 225 230 235 240
 Arg Ser Ser Ala Met Leu Ala Asp Arg Phe His Met His Thr Val Asn
 245 250 255
 Leu Asp Pro Tyr Ala Glu Asn Val Leu Val Asn Leu Lys Thr Ile Ala
 260 265 270
 Thr Thr Phe Ser Ser Leu
 275

<210> 18

<211> 469

<212> PRT

<213> Chlamydia pneumoniae

<400> 18

Met Gly Pro Gly Ser Val Leu Ser Asn His Ser Lys Glu Ala Gly Gly
 1 5 10 15

Ile Ala Ile Asn Asn Val Ile Ile Asp Phe Ser Glu Ile Val Pro Thr
 20 25 30

Lys Asp Asn Ala Thr Val Ala Pro Pro Thr Leu Lys Leu Val Ser Arg
 35 40 45

Thr Asn Ala Asp Ser Lys Asp Lys Ile Asp Ile Thr Gly Thr Val Thr
 50 55 60

Leu Leu Asp Pro Asn Gly Asn Leu Tyr Gln Asn Ser Tyr Leu Gly Glu
 65 70 75 80

Asp Arg Asp Ile Thr Leu Phe Asn Ile Asp Asn Ser Ala Ser Gly Ala
 85 90 95

Val Thr Ala Thr Asn Val Thr Leu Gln Gly Asn Leu Gly Ala Lys Lys
 100 105 110

39/55

Gly Tyr Leu Gly Thr Trp Asn Leu Asp Pro Asn Ser Ser Gly Ser Lys
 115 120 125
 Ile Ile Leu Lys Trp Thr Phe Asp Lys Tyr Leu Arg Trp Pro Tyr Ile
 130 135 140
 Pro Arg Asp Asn His Phe Tyr Ile Asn Ser Ile Trp Gly Ala Gln Asn
 145 150 155 160
 Ser Leu Val Thr Val Asn Gln Gly Ile Leu Gly Asn Met Leu Asn Asn
 165 170 175
 Ala Arg Phe Glu Asp Pro Ala Phe Asn Asn Phe Trp Ala Ser Ala Ile
 180 185 190
 Gly Ser Phe Leu Arg Lys Glu Val Ser Arg Asn Ser Asp Ser Phe Thr
 195 200 205
 Tyr His Gly Arg Gly Tyr Thr Ala Ala Val Asp Ala Lys Pro Arg Gln
 210 215 220
 Glu Phe Ile Leu Gly Ala Ala Phe Ser Gln Val Phe Gly His Ala Glu
 225 230 235 240
 Ser Glu Tyr His Leu Asp Asn Tyr Lys His Lys Gly Ser Gly His Ser
 245 250 255
 Thr Gln Ala Ser Leu Tyr Ala Gly Asn Ile Phe Tyr Phe Pro Ala Ile
 260 265 270
 Arg Ser Arg Pro Ile Leu Phe Gln Gly Val Ala Thr Tyr Gly Tyr Met
 275 280 285
 Gln His Asp Thr Thr Thr Tyr Tyr Pro Ser Ile Glu Glu Lys Asn Met
 290 295 300
 Ala Asn Trp Asp Ser Ile Ala Trp Leu Phe Asp Leu Arg Phe Ser Val
 305 310 315 320
 Asp Leu Lys Glu Pro Gln Pro His Ser Thr Ala Arg Leu Thr Phe Tyr
 325 330 335
 Thr Glu Ala Glu Tyr Thr Arg Ile Arg Gln Glu Lys Phe Thr Glu Leu
 340 345 350
 Asp Tyr Asp Pro Arg Ser Phe Ser Ala Cys Ser Tyr Gly Asn Leu Ala
 355 360 365
 Ile Pro Thr Gly Phe Ser Val Asp Gly Ala Leu Ala Trp Arg Glu Ile
 370 375 380
 Ile Leu Tyr Asn Lys Val Ser Ala Ala Tyr Leu Pro Val Ile Leu Arg
 385 390 395 400

40/55

Asn Asn Pro Lys Ala Thr Tyr Glu Val Leu Ser Thr Lys Glu Lys Gly
 405 410 415

Asn Val Val Asn Val Leu Pro Thr Arg Asn Ala Ala Arg Ala Glu Val
 420 425 430

Ser Ser Gln Ile Tyr Leu Gly Ser Tyr Trp Thr Leu Tyr Gly Thr Tyr
 435 440 445

Thr Ile Asp Ala Ser Met Asn Thr Leu Val Gln Met Ala Asn Gly Gly
 450 455 460

Ile Arg Phe Val Phe
 465

<210> 19

<211> 922

<212> PRT

<213> Chlamydia pneumoniae

<400> 19

Met Arg Phe Ser Leu Cys Gly Phe Pro Leu Val Phe Ser Phe Thr Leu
 1 5 10 15

Leu Ser Val Phe Asp Thr Ser Leu Ser Ala Thr Thr Ile Ser Leu Thr
 20 25 30

Pro Glu Asp Ser Phe His Gly Asp Ser Gln Asn Ala Glu Arg Ser Tyr
 35 40 45

Asn Val Gln Ala Gly Asp Val Tyr Ser Leu Thr Gly Asp Val Ser Ile
 50 55 60

Ser Asn Val Asp Asn Ser Ala Leu Asn Lys Ala Cys Phe Asn Val Thr
 65 70 75 80

Ser Gly Ser Val Thr Phe Ala Gly Asn His His Gly Leu Tyr Phe Asn
 85 90 95

Asn Ile Ser Ser Gly Thr Thr Lys Glu Gly Ala Val Leu Cys Cys Gln
 100 105 110

Asp Pro Gln Ala Thr Ala Arg Phe Ser Gly Phe Ser Thr Leu Ser Phe
 115 120 125

Ile Gln Ser Pro Gly Asp Ile Lys Glu Gln Gly Cys Leu Tyr Ser Lys
 130 135 140

Asn Ala Leu Met Leu Leu Asn Asn Tyr Val Val Arg Phe Glu Gln Asn
 145 150 155 160

Gln Ser Lys Thr Lys Gly Gly Ala Ile Ser Gly Ala Asn Val Thr Ile
 165 170 175

41/55

Val Gly Asn Tyr Asp Ser Val Ser Phe Tyr Gln Asn Ala Ala Thr Phe
 180 185 190
 Gly Gly Ala Ile His Ser Ser Gly Pro Leu Gln Ile Ala Val Asn Gln
 195 200 205
 Ala Glu Ile Arg Phe Ala Gln Asn Thr Ala Lys Asn Gly Ser Gly Gly
 210 215 220
 Ala Leu Tyr Ser Asp Gly Asp Ile Asp Ile Asp Gln Asn Ala Tyr Val
 225 230 235 240
 Leu Phe Arg Glu Asn Glu Ala Leu Thr Thr Ala Ile Gly Lys Gly Gly
 245 250 255
 Ala Val Cys Cys Leu Pro Thr Ser Gly Ser Ser Thr Pro Val Pro Ile
 260 265 270
 Val Thr Phe Ser Asp Asn Lys Gln Leu Val Phe Glu Arg Asn His Ser
 275 280 285
 Ile Met Gly Gly Gly Ala Ile Tyr Ala Arg Lys Leu Ser Ile Ser Ser
 290 295 300
 Gly Gly Pro Thr Leu Phe Ile Asn Asn Ile Ser Tyr Ala Asn Ser Gln
 305 310 315 320
 Asn Leu Gly Gly Ala Ile Ala Ile Asp Thr Gly Gly Glu Ile Ser Leu
 325 330 335
 Ser Ala Glu Lys Gly Thr Ile Thr Phe Gln Gly Asn Arg Thr Ser Leu
 340 345 350
 Pro Phe Leu Asn Gly Ile His Leu Leu Gln Asn Ala Lys Phe Leu Lys
 355 360 365
 Leu Gln Ala Arg Asn Gly Tyr Ser Ile Glu Phe Tyr Asp Pro Ile Thr
 370 375 380
 Ser Glu Ala Asp Gly Ser Thr Gln Leu Asn Ile Asn Gly Asp Pro Lys
 385 390 395 400
 Asn Lys Glu Tyr Thr Gly Thr Ile Leu Phe Ser Gly Glu Lys Ser Leu
 405 410 415
 Ala Asn Asp Pro Arg Asp Phe Lys Ser Thr Ile Pro Gln Asn Val Asn
 420 425 430
 Leu Ser Ala Gly Tyr Leu Val Ile Lys Glu Gly Ala Glu Val Thr Val
 435 440 445
 Ser Lys Phe Thr Gln Ser Pro Gly Ser His Leu Val Leu Asp Leu Gly
 450 455 460
 Thr Lys Leu Ile Ala Ser Lys Glu Asp Ile Ala Ile Thr Gly Leu Ala
 465 470 475 480

42/55

Ile Asp Ile Asp Ser Leu Ser Ser Ser Ser Thr Ala Ala Val Ile Lys
 485 490 495
 Ala Asn Thr Ala Asn Lys Gln Ile Ser Val Thr Asp Ser Ile Glu Leu
 500 505 510
 Ile Ser Pro Thr Gly Asn Ala Tyr Glu Asp Leu Arg Met Arg Asn Ser
 515 520 525
 Gln Thr Phe Pro Leu Leu Ser Leu Glu Pro Gly Ala Gly Gly Ser Val
 530 535 540
 Thr Val Thr Ala Gly Asp Phe Leu Pro Val Ser Pro His Tyr Gly Phe
 545 550 555 560
 Gln Gly Asn Trp Lys Leu Ala Trp Thr Gly Thr Gly Asn Lys Val Gly
 565 570 575
 Glu Phe Phe Trp Asp Lys Ile Asn Tyr Lys Pro Arg Pro Glu Lys Glu
 580 585 590
 Gly Asn Leu Val Pro Asn Ile Leu Trp Gly Asn Ala Val Asp Val Arg
 595 600 605
 Ser Leu Met Gln Val Gln Glu Thr His Ala Ser Ser Leu Gln Thr Asp
 610 615 620
 Arg Gly Leu Trp Ile Asp Gly Ile Gly Asn Phe Phe His Val Ser Ala
 625 630 635 640
 Ser Glu Asp Asn Ile Arg Tyr Arg His Asn Ser Gly Gly Tyr Val Leu
 645 650 655
 Ser Val Asn Asn Glu Ile Thr Pro Lys His Tyr Thr Ser Met Ala Phe
 660 665 670
 Ser Gln Leu Phe Ser Arg Asp Lys Asp Tyr Ala Val Ser Asn Asn Glu
 675 680 685
 Tyr Arg Met Tyr Leu Gly Ser Tyr Leu Tyr Gln Tyr Thr Thr Ser Leu
 690 695 700
 Gly Asn Ile Phe Arg Tyr Ala Ser Arg Asn Pro Asn Val Asn Val Gly
 705 710 715 720
 Ile Leu Ser Arg Arg Phe Leu Gln Asn Pro Leu Met Ile Phe His Phe
 725 730 735
 Leu Cys Ala Tyr Gly His Ala Thr Asn Asp Met Lys Thr Asp Tyr Ala
 740 745 750
 Asn Phe Pro Met Val Lys Asn Ser Trp Arg Asn Asn Cys Trp Ala Ile
 755 760 765

43/55

Glu Cys Gly Gly Ser Met Pro Leu Leu Val Phe Glu Asn Gly Arg Leu
770 775 780

Phe Gln Gly Ala Ile Pro Phe Met Lys Leu Gln Leu Val Tyr Ala Tyr
785 790 795 800

His Gly Asp Phe Lys Glu Thr Thr Ala Asp Gly Arg Arg Phe Ser Asn
805 810 815

Gly Ser Leu Thr Ser Ile Ser Val Pro Leu Gly Ile Arg Phe Glu Lys
820 825 830

Leu Ala Leu Ser Gln Asp Val Leu Tyr Asp Phe Ser Phe Ser Tyr Ile
835 840 845

Pro Asp Ile Phe Arg Lys Asp Pro Ser Cys Glu Ala Ala Leu Val Ile
850 855 860

Ser Gly Asp Ser Trp Leu Val Pro Ala Ala His Val Ser Arg His Ala
865 870 875 880

Phe Val Gly Ser Gly Thr Gly Arg Tyr His Phe Asn Asp Tyr Thr Glu
885 890 895

Leu Leu Cys Arg Gly Ser Ile Glu Cys Arg Pro His Ala Arg Asn Tyr
900 905 910

Asn Ile Asn Cys Gly Ser Lys Phe Arg Phe
915 920

<210> 20

<211> 375

<212> PRT

<213> Chlamydia pneumoniae

<400> 20

Met Pro Ser Ser Trp Lys Arg Leu Leu Gln Val Leu Ser His Lys Ile
1 5 10 15

Ala Ala Thr Glu Ser Gly Gly Gly Ile Tyr Ala Lys Asp Ile Gln Leu
20 25 30

Gln Ala Leu Pro Gly Ser Phe Thr Ile Thr Asp Asn Lys Val Glu Thr
35 40 45

Ser Leu Thr Thr Ser Thr Asn Leu Tyr Gly Gly Gly Ile Tyr Ser Ser
50 55 60

Gly Ala Val Thr Leu Thr Asn Ile Ser Gly Thr Phe Gly Ile Thr Gly
65 70 75 80

Asn Ser Val Ile Asn Thr Ala Thr Ser Gln Asp Ala Asp Ile Gln Gly
85 90 95

44/55

Gly Gly Ile Tyr Ala Thr Thr Ser Leu Ser Ile Asn Gln Cys Asn Thr
 100 105 110
 Pro Ile Leu Phe Ser Asn Asn Ser Ala Ala Thr Lys Lys Thr Ser Thr
 115 120 125
 Thr Lys Gln Ile Ala Gly Gly Ala Ile Phe Ser Ala Ala Val Thr Ile
 130 135 140
 Glu Asn Asn Ser Gln Pro Ile Ile Phe Leu Asn Asn Ser Ala Lys Ser
 145 150 155 160
 Glu Ala Thr Thr Ala Ala Thr Ala Gly Asn Lys Asp Ser Cys Gly Gly
 165 170 175
 Ala Ile Ala Ala Asn Ser Val Thr Leu Thr Asn Asn Pro Glu Ile Thr
 180 185 190
 Phe Lys Gly Asn Tyr Ala Glu Thr Gly Gly Ala Ile Gly Cys Ile Asp
 195 200 205
 Leu Thr Asn Gly Ser Pro Pro Arg Lys Val Ser Ile Ala Asp Asn Gly
 210 215 220
 Ser Val Leu Phe Gln Asp Asn Ser Ala Leu Asn Arg Gly Gly Ala Ile
 225 230 235 240
 Tyr Gly Glu Thr Ile Asp Ile Ser Arg Thr Gly Ala Thr Phe Ile Gly
 245 250 255
 Asn Ser Ser Lys His Asp Gly Ser Ala Ile Cys Cys Ser Thr Ala Leu
 260 265 270
 Thr Leu Ala Pro Asn Ser Gln Leu Ile Phe Glu Asn Asn Lys Val Thr
 275 280 285
 Glu Thr Thr Ala Thr Thr Lys Ala Ser Ile Asn Asn Leu Gly Ala Ala
 290 295 300
 Ile Tyr Gly Asn Asn Glu Thr Ser Asp Val Thr Ile Ser Leu Ser Ala
 305 310 315 320
 Glu Asn Gly Ser Ile Phe Phe Lys Asn Asn Leu Cys Thr Ala Thr Asn
 325 330 335
 Lys Tyr Cys Ser Ile Ala Gly Asn Val Lys Phe Thr Ala Ile Glu Ala
 340 345 350
 Ser Ala Gly Lys Ala Ile Ser Phe Tyr Asp Ala Val Asn Val Pro Pro
 355 360 365
 Lys Lys Gln Leu Leu Lys Ser
 370 375

45/55

<210> 21

<211> 871

<212> PRT

<213> Chlamydia pneumoniae

<400> 21

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Met Lys Tyr Ser Leu Pro Trp Leu Leu Thr Ser Ser Ala Leu Val Phe
  1             5             10             15

Ser Leu His Pro Leu Met Ala Ala Asn Thr Asp Leu Ser Ser Ser Asp
          20             25             30

Asn Tyr Glu Asn Gly Ser Ser Gly Ser Ala Ala Phe Thr Ala Lys Glu
          35             40             45

Thr Ser Asp Ala Ser Gly Thr Thr Tyr Thr Leu Thr Ser Asp Val Ser
  50             55             60

Ile Thr Asn Val Ser Ala Ile Thr Pro Ala Asp Lys Ser Cys Phe Thr
  65             70             75             80

Asn Thr Gly Gly Ala Leu Ser Phe Val Gly Ala Asp His Ser Leu Val
          85             90             95

Leu Gln Thr Ile Ala Leu Thr His Asp Gly Ala Ala Ile Asn Asn Thr
          100            105            110

Asn Thr Ala Leu Ser Phe Ser Gly Phe Ser Ser Leu Leu Ile Asp Ser
          115            120            125

Ala Pro Ala Thr Gly Thr Ser Gly Gly Lys Gly Ala Ile Cys Val Thr
          130            135            140

Asn Thr Glu Gly Gly Thr Ala Thr Phe Thr Asp Asn Ala Ser Val Thr
          145            150            155            160

Leu Gln Lys Asn Thr Ser Glu Lys Asp Gly Ala Ala Val Ser Ala Tyr
          165            170            175

Ser Ile Asp Leu Ala Lys Thr Thr Thr Ala Ala Leu Leu Asp Gln Asn
          180            185            190

Thr Ser Thr Lys Asn Gly Gly Ala Leu Cys Ser Thr Ala Asn Thr Thr
          195            200            205

Val Gln Gly Asn Ser Gly Thr Val Thr Phe Ser Ser Asn Thr Ala Thr
          210            215            220

Asp Lys Gly Gly Gly Ile Tyr Ser Lys Glu Lys Asp Ser Thr Leu Asp
          225            230            235            240

Ala Asn Thr Gly Val Val Thr Phe Lys Ser Asn Thr Ala Lys Thr Gly
          245            250            255

Gly Ala Trp Ser Ser Asp Asp Asn Leu Ala Leu Thr Gly Asn Thr Gln
          260            265            270

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46/55

Val Leu Phe Gln Glu Asn Lys Thr Thr Gly Ser Ala Ala Gln Ala Asn
 275 280 285
 Asn Pro Glu Gly Cys Gly Gly Ala Ile Cys Cys Tyr Leu Ala Thr Ala
 290 295 300
 Thr Asp Lys Thr Gly Leu Ala Ile Ser Gln Asn Gln Glu Met Ser Phe
 305 310 315 320
 Thr Ser Asn Thr Thr Thr Ala Asn Gly Gly Ala Ile Tyr Ala Thr Lys
 325 330 335
 Cys Thr Leu Asp Gly Asn Thr Thr Leu Thr Phe Asp Gln Asn Thr Ala
 340 345 350
 Thr Ala Gly Cys Gly Gly Ala Ile Tyr Thr Glu Thr Glu Asp Phe Ser
 355 360 365
 Leu Lys Gly Ser Thr Gly Thr Val Thr Phe Ser Thr Asn Thr Ala Lys
 370 375 380
 Thr Gly Gly Ala Leu Tyr Ser Lys Gly Asn Ser Ser Leu Thr Gly Asn
 385 390 395 400
 Thr Asn Leu Leu Phe Ser Gly Asn Lys Ala Thr Gly Pro Ser Asn Ser
 405 410 415
 Ser Ala Asn Gln Glu Gly Cys Gly Gly Ala Ile Leu Ala Phe Ile Asp
 420 425 430
 Ser Gly Ser Val Ser Asp Lys Thr Gly Leu Ser Ile Ala Asn Asn Gln
 435 440 445
 Glu Val Ser Leu Thr Ser Asn Ala Ala Thr Val Ser Gly Gly Ala Ile
 450 455 460
 Tyr Ala Thr Lys Cys Thr Leu Thr Gly Asn Gly Ser Leu Thr Phe Asp
 465 470 475 480
 Gly Asn Thr Ala Gly Thr Ser Gly Gly Ala Ile Tyr Thr Glu Thr Glu
 485 490 495
 Asp Phe Thr Leu Thr Gly Ser Thr Gly Thr Val Thr Phe Ser Thr Asn
 500 505 510
 Thr Ala Lys Thr Gly Gly Ala Leu Tyr Ser Lys Gly Asn Asn Ser Leu
 515 520 525
 Ser Gly Asn Thr Asn Leu Leu Phe Ser Gly Asn Lys Ala Thr Gly Pro
 530 535 540
 Ser Asn Ser Ser Ala Asn Gln Glu Gly Cys Gly Gly Ala Ile Leu Ser
 545 550 555 560

47/55

Phe Leu Glu Ser Ala Ser Val Ser Thr Lys Lys Gly Leu Trp Ile Glu
 565 570 575
 Asp Asn Glu Asn Val Ser Leu Ser Gly Asn Thr Ala Thr Val Ser Gly
 580 585 590
 Gly Ala Ile Tyr Ala Thr Lys Cys Ala Leu His Gly Asn Thr Thr Leu
 595 600 605
 Thr Phe Asp Gly Asn Thr Ala Glu Thr Ala Gly Gly Ala Ile Tyr Thr
 610 615 620
 Glu Thr Glu Asp Phe Thr Leu Thr Gly Ser Thr Gly Thr Val Thr Phe
 625 630 635 640
 Ser Thr Asn Thr Ala Lys Thr Ala Gly Ala Leu His Thr Lys Gly Asn
 645 650 655
 Thr Ser Phe Thr Lys Asn Lys Ala Leu Val Phe Ser Gly Asn Ser Ala
 660 665 670
 Thr Ala Thr Ala Thr Thr Thr Thr Asp Gln Glu Gly Cys Gly Gly Ala
 675 680 685
 Ile Leu Cys Asn Ile Ser Glu Ser Asp Ile Ala Thr Lys Ser Leu Thr
 690 695 700
 Leu Thr Glu Asn Glu Ser Leu Ser Phe Ile Asn Asn Thr Ala Lys Arg
 705 710 715 720
 Ser Gly Gly Gly Ile Tyr Ala Pro Lys Cys Val Ile Ser Gly Ser Glu
 725 730 735
 Ser Ile Asn Phe Asp Gly Asn Thr Ala Glu Thr Ser Gly Gly Ala Ile
 740 745 750
 Tyr Ser Lys Asn Leu Ser Ile Thr Ala Asn Gly Pro Val Ser Phe Thr
 755 760 765
 Asn Asn Ser Gly Gly Lys Gly Gly Ala Ile Tyr Ile Ala Asp Ser Gly
 770 775 780
 Glu Leu Ser Leu Glu Ala Ile Asp Gly Asp Ile Thr Phe Ser Gly Asn
 785 790 795 800
 Arg Ala Thr Glu Gly Thr Ser Thr Pro Asn Ser Ile His Leu Gly Ala
 805 810 815
 Arg Gly Lys Ile Thr Lys Leu Ala Ala Ala Pro Gly His Thr Ile Tyr
 820 825 830
 Phe Tyr Asp Pro Ile Thr Met Glu Ala Pro Ala Ser Gly Gly Thr Ile
 835 840 845
 Glu Glu Leu Val Ile Asn Pro Val Val Lys Ala Ile Val Pro Pro Pro
 850 855 860

48/55

Gln Pro Lys Asn Gly Pro Ile
865 870

<210> 22

<211> 963

<212> PRT

<213> Chlamydia pneumoniae

<400> 22

Met Thr Asn Ser Ile Phe Ile Ser Lys Phe Gly Cys Leu Cys Asp Pro
1 5 10 15

Phe Val Ser Ala Phe Tyr Pro Thr Ala Leu Cys Cys Ser Leu Ser Gly
20 25 30

Asn Glu Val Pro Asn Leu Ala Ser Cys Gln Met Ser Arg Lys Asp Ile
35 40 45

Ser Ala Phe His Thr Ser Pro Ser Phe Arg Leu Asn Val Thr Pro Glu
50 55 60

Pro Leu Val Ser Ser Phe Arg Pro Ser Asn Leu Leu Asn Gly Phe Gly
65 70 75 80

His Asp Ile Thr Gln Asp Ile Thr Ile Thr Gly Asn Ser Ile Asn Ser
85 90 95

Val Ile Asp Tyr Asn Tyr His Tyr Glu Asp Gly Gly Ile Leu Ala Cys
100 105 110

Lys Asn Leu Phe Ile Ser Glu Asn Lys Gly Asn Leu Ser Phe Glu Arg
115 120 125

Asn Ser Ser His Ser Ser Gly Gly Ala Leu Tyr Ser Val Arg Glu Cys
130 135 140

Trp Ile Ser Lys Asn Gln Asn Tyr Ser Phe Ile Ser Asn Ala Ala Ser
145 150 155 160

Leu Ala Thr Thr Thr Thr Ser Gly Phe Gly Gly Ala Ile His Ala Leu
165 170 175

Asp Ser Tyr Ile Thr Asn Asn Leu Gly Glu Gly Gln Phe Leu Asp Asn
180 185 190

Val Ser Lys Asn Arg Gly Gly Ala Ile Tyr Val Gly Val Ser Leu Ser
195 200 205

Ile Thr Asp Asn Leu Gly Pro Ile Val Ile Lys Lys Asn Gln Thr Leu
210 215 220

Glu Asp Ser Ser Phe Gly Gly Gly Ile Phe Cys Arg Ala Val Asn Ile
225 230 235 240

49/55

Glu Arg Asn Tyr Gln Asn Ile Gln Ile Asn Asp Asn Ala Ser Gly Gln
 245 250 255
 Gly Val Val Tyr Phe Leu Pro Leu Gly Val Ile Ile Ser Ser Asn Lys
 260 265 270
 Glu Ile Ile Glu Ile Ser Asn His Ser Ala Ser Ser Ile Asn Thr Ala
 275 280 285
 Ser Gly Lys Leu Tyr Pro Gly Gly Gly Gly Ile Met Cys Thr Ser Leu
 290 295 300
 Ser His Glu Asn Asn Pro Lys Gly Leu Ile Phe Asn Asn Lys Thr Ala
 305 310 315 320
 Ala Leu Ser Gly Gly Val Tyr Thr Arg Asp Leu Ser Ser Ser Lys Ile
 325 330 335
 Thr Val Arg Thr Ala Phe Ile Asn Asn Ser Ala Thr Ser Gly Gly Ala
 340 345 350
 Leu Ile Asn Leu Ser Gly Ile Gly Ser Thr Pro Gln Asn Phe Phe Leu
 355 360 365
 Ser Ala Asp Tyr Gly Asp Ile Leu Phe Asn Asn Asn Thr Ile Thr Ser
 370 375 380
 Ser Ser Pro Gln Pro Gly Tyr Arg Asn Ala Leu Tyr Ala Ala Pro Gly
 385 390 395 400
 Ile Asn Leu Lys Leu Gly Ala Arg Gln Gly Tyr Lys Ile Leu Phe Tyr
 405 410 415
 Asp Pro Ile Asp His Asp Gln Thr Thr Thr Asp Pro Ile Val Phe Asn
 420 425 430
 Tyr Glu Pro His His Leu Gly Thr Val Leu Phe Ser Gly Ile Asn Val
 435 440 445
 Asp Ser Asn Ala Thr Asn Pro Leu Asn Phe Leu Ser Lys Phe Ser Asn
 450 455 460
 Ser Ser Arg Leu Glu Arg Gly Val Leu Ala Ile Glu Asp Arg Ala Ala
 465 470 475 480
 Ile Ser Cys Lys Thr Leu Ser Gln Thr Gly Gly Ile Leu Arg Leu Gly
 485 490 495
 Asn Ala Ala Leu Ile Arg Thr Lys Gly Pro Gly Ser Ser Ile Asn Phe
 500 505 510
 Asn Ala Ile Ala Ile Asn Leu Pro Ser Ile Leu Gln Ser Glu Ala Ser
 515 520 525

50/55

Ala Pro Lys Phe Trp Ile Tyr Pro Thr Leu Thr Gly Ser Thr Tyr Ser
530 535 540

Glu Asp Thr Ser Ser Thr Ile Thr Leu Ser Gly Pro Leu Thr Phe Leu
545 550 555 560

Asn Asp Glu Asn Glu Asn Pro Tyr Asp Ser Leu Asp Leu Ser Glu Pro
565 570 575

Arg Lys Asp Ile Pro Pro Pro Leu Pro Pro Arg Cys Asp Cys Lys Lys
580 585 590

Ile Asp Thr Ser Asn Leu Ile Val Glu Ala Met Asn Leu Asp Glu His
595 600 605

Tyr Gly Tyr Gln Gly Ile Trp Ser Pro Tyr Trp Met Glu Thr Thr Thr
610 615 620

Thr Thr Ser Ser Thr Val Pro Glu Gln Thr Asn Thr Asn His Arg Gln
625 630 635 640

Leu Tyr Val Asp Trp Thr Pro Val Gly Tyr Arg Pro Asn Pro Glu Arg
645 650 655

His Gly Glu Phe Ile Ala Asn Thr Leu Trp Gln Ser Ala Tyr Asn Ala
660 665 670

Leu Leu Gly Ile Arg Ile Leu Pro Pro Gln Asn Leu Lys Glu His Asp
675 680 685

Leu Glu Ala Ser Leu Gln Gly Leu Gly Leu Leu Ile Asn Gln His Asn
690 695 700

Arg Glu Gly Arg Lys Gly Phe Arg Asn His Thr Thr Gly Tyr Ala Ala
705 710 715 720

Thr Thr Ser Ala Lys Thr Ala Ala Arg His Ser Phe Ser Leu Gly Phe
725 730 735

Ala Gln Met Phe Ser Lys Thr Arg Glu Arg Gln Ser Pro Ser Thr Thr
740 745 750

Ser Ser His Asn Tyr Phe Ala Gly Leu Arg Phe Asp Ser Leu Leu Phe
755 760 765

Arg Asp Phe Ile Ser Thr Gly Leu Ser Leu Gly Tyr Ser Tyr Gly Asp
770 775 780

His His Met Leu Cys His Tyr Thr Glu Ile Leu Lys Gly Ser Ser Lys
785 790 795 800

Ala Phe Phe Asn Asn His Thr Leu Val Ala Ser Leu Asp Cys Thr Phe
805 810 815

Leu Pro Ala Arg Ile Thr Arg Thr Leu Glu Leu Gln Pro Phe Ile Ser
820 825 830

51/55

Ala Ile Ala Leu Arg Cys Ser Gln Ala Ser Phe Gln Glu Thr Gly Asp
835 840 845

His Ile Arg Lys Phe His Pro Lys His Pro Leu Thr Asp Leu Ser Ser
850 855 860

Pro Ile Gly Phe Arg Ser Glu Trp Lys Thr Ser His His Ile Pro Met
865 870 875 880

Leu Trp Thr Thr Glu Ile Ser Tyr Val Pro Thr Leu Tyr Arg Lys Asn
885 890 895

Pro Glu Met Phe Thr Thr Leu Leu Ile Ser Asn Gly Thr Trp Thr Thr
900 905 910

Gln Ala Thr Pro Val Ser Tyr Asn Ser Val Ala Ala Lys Ile Lys Asn
915 920 925

Thr Ser Gln Leu Phe Ser Arg Val Thr Leu Ser Leu Asp Tyr Ser Ala
930 935 940

Gln Val Ser Ser Ser Thr Val Gly Gln Tyr Leu Lys Ala Glu Ser His
945 950 955 960

Cys Thr Phe

<210> 23

<211> 514

<212> PRT

<213> Chlamydia pneumoniae

<400> 23

Met Thr Ile Leu Arg Asn Phe Leu Thr Cys Ser Ala Leu Phe Leu Ala
1 5 10 15

Leu Pro Ala Ala Ala Gln Val Val Tyr Leu His Glu Ser Asp Gly Tyr
20 25 30

Asn Gly Ala Ile Asn Asn Lys Ser Leu Glu Pro Lys Ile Thr Cys Tyr
35 40 45

Pro Glu Gly Thr Ser Tyr Ile Phe Leu Asp Asp Val Arg Ile Ser Asn
50 55 60

Val Lys His Asp Gln Glu Asp Ala Gly Val Phe Ile Asn Arg Ser Gly
65 70 75 80

Asn Leu Phe Phe Met Gly Asn Arg Cys Asn Phe Thr Phe His Asn Leu
85 90 95

Met Thr Glu Gly Phe Gly Ala Ala Ile Ser Asn Arg Val Gly Asp Thr
100 105 110

52/55

Thr Leu Thr Leu Ser Asn Phe Ser Tyr Leu Ala Phe Thr Ser Ala Pro
 115 120 125
 Leu Leu Pro Gln Gly Gln Gly Ala Ile Tyr Ser Leu Gly Ser Val Met
 130 135 140
 Ile Glu Asn Ser Glu Glu Val Thr Phe Cys Gly Asn Tyr Ser Ser Trp
 145 150 155 160
 Ser Gly Ala Ala Ile Tyr Thr Pro Tyr Leu Leu Gly Ser Lys Ala Ser
 165 170 175
 Arg Pro Ser Val Asn Leu Ser Gly Asn Arg Tyr Leu Val Phe Arg Asp
 180 185 190
 Asn Val Ser Gln Val Tyr Gly Gly Ala Ile Ser Thr His Asn Leu Thr
 195 200 205
 Leu Thr Thr Arg Gly Pro Ser Cys Phe Glu Asn Asn His Ala Tyr His
 210 215 220
 Asp Val Asn Ser Asn Gly Gly Ala Ile Ala Ile Ala Pro Gly Gly Ser
 225 230 235 240
 Ile Ser Ile Ser Val Lys Ser Gly Asp Leu Ile Phe Lys Gly Asn Thr
 245 250 255
 Ala Ser Gln Asp Gly Asn Thr Ile His Asn Ser Ile His Leu Gln Ser
 260 265 270
 Gly Ala Gln Phe Lys Asn Leu Arg Ala Val Ser Glu Ser Gly Val Tyr
 275 280 285
 Phe Tyr Asp Pro Ile Ser His Ser Glu Ser His Lys Ile Thr Asp Leu
 290 295 300
 Val Ile Asn Ala Pro Glu Gly Lys Glu Thr Tyr Glu Gly Thr Ile Ser
 305 310 315 320
 Phe Ser Gly Leu Cys Leu Asp Asp His Glu Val Cys Ala Glu Asn Leu
 325 330 335
 Thr Ser Thr Ile Leu Gln Asp Val Thr Leu Ala Gly Gly Thr Leu Ser
 340 345 350
 Leu Ser Asp Gly Val Thr Leu Gln Leu His Ser Phe Lys Gln Glu Ala
 355 360 365
 Ser Ser Thr Leu Thr Met Ser Pro Gly Thr Thr Leu Leu Cys Ser Gly
 370 375 380
 Asp Ala Arg Val Gln Asn Leu His Ile Leu Ile Glu Asp Thr Asp Asn
 385 390 395 400
 Phe Val Pro Val Arg Ile Arg Ala Glu Asp Lys Asp Ala Leu Val Ser
 405 410 415

53/55

Leu Glu Lys Leu Lys Val Ala Phe Glu Ala Tyr Trp Ser Val Tyr Asp
 420 425 430

Phe Pro Gln Phe Lys Glu Ala Phe Thr Ile Pro Leu Leu Glu Leu Leu
 435 440 445

Gly Pro Ser Phe Asp Ser Leu Leu Leu Gly Glu Thr Thr Leu Glu Arg
 450 455 460

Thr Gln Val Thr Thr Glu Asn Asp Ala Val Arg Gly Phe Trp Ser Leu
 465 470 475 480

Ser Trp Glu Glu Tyr Pro Pro Ser Leu Asp Lys Asp Arg Arg Ile Thr
 485 490 495

Pro Thr Lys Lys Thr Val Phe Leu Thr Trp Asn Pro Glu Ile Thr Ser
 500 505 510

Thr Pro

<210> 24
 <211> 289
 <212> PRT
 <213> Chlamydia pneumoniae

<400> 24
 Met Gly Ile Ser Leu Pro Glu Leu Phe Ser Asn Leu Gly Ser Ala Tyr
 1 5 10 15

Leu Asp Tyr Ile Phe Gln His Pro Pro Ala Tyr Val Trp Ser Val Phe
 20 25 30

Leu Leu Leu Leu Ala Arg Leu Leu Pro Ile Phe Ala Val Ala Pro Phe
 35 40 45

Leu Gly Ala Lys Leu Phe Pro Ser Pro Ile Lys Ile Gly Ile Ser Leu
 50 55 60

Ser Trp Leu Ala Ile Ile Phe Pro Lys Val Leu Ala Asp Thr Gln Ile
 65 70 75 80

Thr Asn Tyr Met Asp Asn Asn Leu Phe Tyr Val Leu Leu Val Lys Glu
 85 90 95

Met Ile Ile Gly Ile Val Ile Gly Phe Val Leu Ala Phe Pro Phe Tyr
 100 105 110

Ala Ala Gln Ser Ala Gly Ser Phe Ile Thr Asn Gln Gln Gly Ile Gln
 115 120 125

Gly Leu Glu Gly Ala Thr Ser Leu Ile Ser Ile Glu Gln Thr Ser Pro
 130 135 140

55/55

Ile Phe Leu Pro Ala Ser Ser Ala Asn Ala Ile Leu Tyr Tyr Thr Gly
 115 120 125
 Pro Val Lys Ile Ala Leu Ile Asn Cys Leu Gly Leu Tyr Ser Ile Ala
 130 135 140
 Lys Glu Leu Lys His Ile Leu Asp Lys Val Val Ile Glu Arg Val Lys
 145 150 155 160
 Asn Ala Leu Ser Pro Thr Glu Lys Leu Phe Leu Thr Tyr Cys Gln Ser
 165 170 175
 His Pro Met Lys His Leu Glu Thr Thr Asn Phe Leu Ser Ser Trp Thr
 180 185 190
 Thr Asp Ala Glu Leu Arg Gln Phe Val His Lys Gln Gly Leu Glu Phe
 195 200 205
 Leu Gly Lys Ala Leu Thr Lys Glu Asn Ala Ser Phe Leu Trp Tyr Phe
 210 215 220
 Leu Arg Arg Leu Asp Val Gly Arg Ala Tyr Ile Val Glu Gln Thr Leu
 225 230 235 240
 Lys Thr Trp Tyr Asp His Pro Tyr Val Asp Tyr Phe Lys Ser Arg Leu
 245 250 255
 Glu Gln Cys Met Lys Val Leu Val Lys
 260 265
 <210> 26
 <211> 95
 <212> PRT
 <213> Chlamydia pneumoniae
 <400> 26
 Met Leu Ala Phe Phe Ala Thr Ser Phe Lys Ser Val Leu Phe Glu Tyr
 1 5 10 15
 Ser Tyr Gln Ser Leu Leu Leu Ile Leu Ile Val Ser Ala Pro Pro Ile
 20 25 30
 Ile Leu Ala Ser Ile Val Gly Ile Met Val Ala Ile Phe Gln Ala Ala
 35 40 45
 Thr Gln Ile Gln Glu Gln Thr Phe Ala Phe Ala Val Lys Leu Val Val
 50 55 60
 Ile Phe Gly Thr Leu Met Ile Ser Gly Gly Trp Leu Ser Asn Met Ile
 65 70 75 80
 Leu Arg Phe Ala Gly Gln Ile Phe Gln Asn Phe Tyr Lys Trp Lys
 85 90 95